



SEQUENCE LISTING

<110> Tillet, D
Thomas, T

<120> A method of sequestering and/or purifying a polypeptide

<140> 10/785,452

<141> 2004-02-25

<150> Australia PCT/AU02/01159
Australia 2002322186

<151> 2002-08-27

<160> 12

<210> 1

<211> 714

<212> DNA

<213> Aequorea victoria

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Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	Gln	Lys	Phe	Ser	Val	Ser	
				20					25					30	

gga	gag	ggt	gaa	ggt	gat	gca	aca	tac	gga	aaa	ctt	acc	ctt	aaa	135
Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	
				35					40					45	

ttt	att	tgc	act	act	ggg	aag	cta	cct	gtt	cca	tgg	cca	aca	ctt	180
Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	
				50					55					60	

gtc	act	act	ttc	gcg	tat	ggt	ctt	caa	tgc	ttt	gcg	aga	tac	cca	225
Val	Thr	Thr	Phe	Ala	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	
				65					70					75	

gat	cat	atg	aaa	cag	cat	gac	ttt	ttc	aag	agt	gcc	atg	ccc	gaa	270
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	
				80					85					90	
ggt	tat	gta	cag	gaa	aga	act	ata	ttt	tac	aaa	gat	gac	ggg	aac	315
Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Tyr	Lys	Asp	Asp	Gly	Asn	
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Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	
				110					115					120	
aat	aga	atc	gag	tta	aaa	ggt	att	gat	ttt	aaa	gaa	gat	gga	aac	405
Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	
				125					130					135	
att	ctt	gga	cac	aaa	atg	gaa	tac	aac	tat	aac	tca	cat	aat	gta	450
Ile	Leu	Gly	His	Lys	Met	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	
				140					145					150	
tac	atc	atg	gca	gac	aaa	cca	aag	aat	gga	atc	aaa	ggt	aac	ttc	495
Tyr	Ile	Met	Ala	Asp	Lys	Pro	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	
				155					160					165	
aaa	att	aga	cac	aac	att	aaa	gat	gga	agc	ggt	caa	tta	gca	gac	540
Lys	Ile	Arg	His	Asn	Ile	Lys	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	
				170					175					180	
cat	tat	caa	caa	aat	act	cca	att	ggc	gat	ggc	cct	gtc	ctt	tta	585
His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	
				185					190					195	
cca	gac	aac	cat	tac	ctg	tcc	aca	caa	tct	gcc	ctt	tcc	aaa	gat	630
Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	
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ccc	aac	gaa	aag	aga	gat	cac	atg	atc	ctt	ctt	gag	ttt	gta	aca	675
Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Ile	Leu	Leu	Glu	Phe	Val	Thr	
				215					220					225	
gct	gct	ggg	att	aca	cat	ggc	atg	gat	gaa	cta	tac	aaa			714
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<212> DNA

<213> Escherichia coli

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Arg	Glu	Arg	Ile	Glu	Gly	Val	Glu	Phe	Phe	Ala	Val	Asn	Thr	Asp	
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Ala	Gln	Ala	Leu	Arg	Lys	Thr	Ala	Val	Gly	Gln	Thr	Ile	Gln	Ile	
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ggc	agc	ggc	atc	acc	aaa	gga	ctg	ggc	gct	ggc	gct	aat	cca	gaa	225
Gly	Ser	Gly	Ile	Thr	Lys	Gly	Leu	Gly	Ala	Gly	Ala	Asn	Pro	Glu	
				65					70					75	
gtt	ggc	cgc	aat	gcg	gct	gat	gag	gat	cgc	gat	gca	ttg	cgt	gcg	270
Val	Gly	Arg	Asn	Ala	Ala	Asp	Glu	Asp	Arg	Asp	Ala	Leu	Arg	Ala	
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ggc	ggc	acc	ggc	aca	ggc	gcg	gca	cca	gtc	gtc	gct	gaa	gtg	gca	360
Gly	Gly	Thr	Gly	Thr	Gly	Ala	Ala	Pro	Val	Val	Ala	Glu	Val	Ala	
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aaa	gat	ttg	ggc	atc	ctg	acc	gtt	gct	gtc	gtc	act	aag	cct	ttc	405
Lys	Asp	Leu	Gly	Ile	Leu	Thr	Val	Ala	Val	Val	Thr	Lys	Pro	Phe	
				125					130					135	

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Asn	Phe	Glu	Gly	Lys	Lys	Arg	Met	Ala	Phe	Ala	Glu	Gln	Gly	Ile	
				140					145					150	
act	gaa	ctg	tcc	aag	cat	gtg	aac	tct	ctg	atc	act	atc	ccg	aac	495
Thr	Glu	Leu	Ser	Lys	His	Val	Asn	Ser	Leu	Ile	Thr	Ile	Pro	Asn	
				155					160					165	
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Asp	Lys	Leu	Leu	Lys	Val	Leu	Gly	Arg	Gly	Ile	Ser	Leu	Leu	Asp	
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Ala	Phe	Gly	Ala	Ala	Asn	Asp	Val	Leu	Lys	Gly	Ala	Val	Gln	Gly	
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Ile	Ala	Glu	Leu	Ile	Thr	Arg	Pro	Gly	Leu	Met	Asn	Val	Asp	Phe	
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Gly	Ser	Gly	Val	Ala	Ser	Gly	Glu	Asp	Arg	Ala	Glu	Glu	Ala	Ala	
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gaa	atg	gct	atc	tct	tct	ccg	ctg	ctg	gaa	gat	atc	gac	ctg	tct	765
Glu	Met	Ala	Ile	Ser	Ser	Pro	Leu	Leu	Glu	Asp	Ile	Asp	Leu	Ser	
				245					250					255	
ggc	gcg	cgc	ggc	gtg	ctg	gtt	aac	atc	acg	gcg	ggc	ttc	gac	ctg	810
Gly	Ala	Arg	Gly	Val	Leu	Val	Asn	Ile	Thr	Ala	Gly	Phe	Asp	Leu	
				260					265					270	
cgt	ctg	gat	gag	ttc	gaa	acg	gta	ggg	aac	acc	atc	cgt	gca	ttt	855
Arg	Leu	Asp	Glu	Phe	Glu	Thr	Val	Gly	Asn	Thr	Ile	Arg	Ala	Phe	
				275					280					285	
gct	tcc	gac	aac	gcg	act	gtg	gtt	atc	ggg	act	tct	ctt	gac	ccg	900
Ala	Ser	Asp	Asn	Ala	Thr	Val	Val	Ile	Gly	Thr	Ser	Leu	Asp	Pro	
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gat	atg	aat	gac	gag	ctg	cgc	gta	acc	gtt	gtt	gcg	aca	ggg	atc	945
Asp	Met	Asn	Asp	Glu	Leu	Arg	Val	Thr	Val	Val	Ala	Thr	Gly	Ile	
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ggc atg gac aaa cgt cct gaa atc act ctg gtg acc aat aag cag 990
 Gly Met Asp Lys Arg Pro Glu Ile Thr Leu Val Thr Asn Lys Gln
 320 325 330

gtt cag cag cca gtg atg gat cgc tac cag cag cat ggg atg gct 1035
 Val Gln Gln Pro Val Met Asp Arg Tyr Gln Gln His Gly Met Ala
 335 340 345

ccg ctg acc caa gag cag aag ccg gtt gct aaa gtc gtg aat gac 1080
 Pro Leu Thr Gln Glu Gln Lys Pro Val Ala Lys Val Val Asn Asp
 350 355 360

aat gcg ccg caa act gcg aaa gag ccg gat tat ctg gat atc cca 1125
 Asn Ala Pro Gln Thr Ala Lys Glu Pro Asp Tyr Leu Asp Ile Pro
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<213> Human rhinovirus

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atg	act	ata	aca	acc	tca	aag	gga	gag	ttc	aca	ggg	tta	ggc	ata	90
Met	Thr	Ile	Thr	Thr	Ser	Lys	Gly	Glu	Phe	Thr	Gly	Leu	Gly	Ile	
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cat	gat	cgt	gtc	tgt	gtg	ata	ccc	aca	cac	gca	cag	cct	ggg	gat	135
His	Asp	Arg	Val	Cys	Val	Ile	Pro	Thr	His	Ala	Gln	Pro	Gly	Asp	
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gat	gta	cta	gtg	aat	ggg	cag	aaa	att	aga	gtt	aag	gat	aag	tac	180
Asp	Val	Leu	Val	Asn	Gly	Gln	Lys	Ile	Arg	Val	Lys	Asp	Lys	Tyr	
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aaa	tta	gta	gat	cca	gag	aac	att	aat	cta	gag	ctt	aca	gtg	ttg	225
Lys	Leu	Val	Asp	Pro	Glu	Asn	Ile	Asn	Leu	Glu	Leu	Thr	Val	Leu	
				65					70					75	
act	tta	gat	aga	aat	gaa	aaa	ttc	aga	gat	atc	agg	gga	ttt	ata	270
Thr	Leu	Asp	Arg	Asn	Glu	Lys	Phe	Arg	Asp	Ile	Arg	Gly	Phe	Ile	
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Ser	Glu	Asp	Leu	Glu	Gly	Val	Asp	Ala	Thr	Leu	Val	Val	His	Ser	
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aat	aac	ttt	acc	aac	act	atc	tta	gaa	gtt	ggc	cct	gta	aca	atg	360
Asn	Asn	Phe	Thr	Asn	Thr	Ile	Leu	Glu	Val	Gly	Pro	Val	Thr	Met	
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gca	gga	ctt	att	aat	ttg	agt	agc	acc	ccc	act	aac	aga	atg	att	405
Ala	Gly	Leu	Ile	Asn	Leu	Ser	Ser	Thr	Pro	Thr	Asn	Arg	Met	Ile	
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cgt	tat	gat	tat	gca	aca	aaa	act	ggg	cag	tgt	gga	ggt	gtg	ctg	450
Arg	Tyr	Asp	Tyr	Ala	Thr	Lys	Thr	Gly	Gln	Cys	Gly	Gly	Val	Leu	
				140					145					150	

tgt	gct	act	ggt	aag	atc	ttt	ggt	att	cat	gtt	ggc	ggt	aat	gga	495
Cys	Ala	Thr	Gly	Lys	Ile	Phe	Gly	Ile	His	Val	Gly	Gly	Asn	Gly	
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aga	caa	gga	ttt	tca	gct	caa	ctt	aaa	aaa	caa	tat	ttt	gta	gag	540
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Lys	Gln	
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